Claims

1. Method for identification of a Gram positive pathogenic organism or a subset of organisms being a member of a predetermined group of pathogenic Gram positive bacteria in a clinical sample comprising

a) isolating a clinical specimen containing at least partially purified nucleic acid,

b) subjecting said clinical specimen to at least one amplification and detection comprising

ba) an amplification step using at least one set of amplification primers capable of amplifying a pre-selected nucleic acid sequence region from a predetermined sub-group of pathogenic Gram positive bacteria to which said Gram positive pathogenic organism belongs,

bb) a detection step using at least one hybridization reagent capable of detecting said pre-selected nucleic acid sequence region from said predetermined sub-group of pathogenic Gram positive bacteria wherein said detection step bb) comprising steps

bba) monitoring hybridization at a pre-selected temperature, said hybridization being indicative for the presence in the sample of at least one species contained in said sub-group, and

bbb) monitoring temperature dependence of hybridization, said temperature dependence being indicative for the presence of at least the species of said pathogenic Gram positive bacterium or said subset of organisms,

c) identifying said organism or said subset of organisms based on the results of the monitoring steps in bb).

2. A method according to claim 1, wherein said sub-group is a genus.

3. A method according to any of claims 1 and 2, wherein the hybridization reagent comprises two probes complementary to adjacent sequences in the target nucleic acid sequence region, one being labelled by a FRET donor, and the other being labelled by a FRET acceptor.

4. A method according to any of claim 1 to 3, wherein said predetermined group of pathogenic Gram positive bacteria comprises the species

5. A method according to any of claims 1 to 4, wherein the predetermined subgroup comprises the species Staphylococcus aureus, Streptococcus preumoniae, Enterococcus faecium and Enterococcus faecalis.

6. A method according to any of claims 1 to 5, wherein the preselected nucleic acid sequence region comprises at least 20 nucleotides of an rRNA spacer region.

7. A method according to any of claims 1 to 6, wherein said amplification and detection is done homogeneously.

8. A method according to any of claims 1 to 7, wherein said species are selected from the genera Staphylococcus, Enterococcus and Streptococcus.

9. A method according to any of claims 1 to 7, wherein said species are selected from one of the genera Staphylococcus.

10. A kit for the identification of a Gram positive pathogenic bacterium selected from the genera Enterococcus, Staphylococcus and Streptococcus containing a set of primers capable of amplifying a sequence of at least 20 nucleotides from the 16S-23S rRNA spacer region of Enterococcus, Staphylococcus and Streptococcus, respectively.